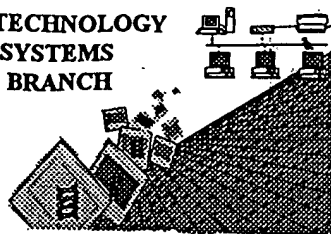# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/029,359 A_

Source: _OIPE_

Date Processed by STIC: _3/27/02_

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
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   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
          Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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Revised 01/29/2002
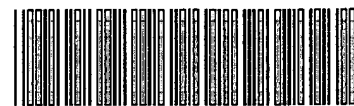
OIPE

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10 029,359A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences (OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences (NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ___ Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

Does Not Comply
Corrected Diskette Needed

Error on p. 2

RAW SEQUENCE LISTING   DATE: 03/27/2002
PATENT APPLICATION: US/10/029,359A   TIME: 13:59:40

Input Set : A:\00404.sequencelist.txt
Output Set: N:\CRF3\03272002\J029359A.raw

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 3 <110> APPLICANT: Pharmacia AB
 5 <120> TITLE OF INVENTION: Protein Cluster II
 7 <130> FILE REFERENCE: 00404
 9 <140> CURRENT APPLICATION NUMBER: US/10/029,359A
11 <141> CURRENT FILING DATE: 2001-12-21
13 <160> NUMBER OF SEQ ID NOS: 6
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 505
19 <212> TYPE: DNA
20 <213> ORGANISM: human
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (21)..(497)
26 <220> FEATURE:
27 <221> NAME/KEY: misc_feature
28 <222> LOCATION: (297)..()
29 <223> OTHER INFORMATION: n=a, g, c or t
31 <400> SEQUENCE: 1
32 gcaagaggga gccacggccg atg aca gaa aat tca ctt tcc gag atg gcc tct       53
33                      Met Thr Glu Asn Ser Leu Ser Glu Met Ala Ser
34                       1               5                  10
36 aaa tcc tgg ctg aat ttt tta acc ttc ctc tat gga tcg gca ata ggg      101
37 Lys Ser Trp Leu Asn Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly
38              15                  20                  25
40 ttt att tta ttt tct cag cta ctt agt att ttg ttg gga gaa gag ggt      149
41 Phe Ile Leu Phe Ser Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly
42          30                  35                  40
44 gac acc cag act aat gtt ctt cat aat gat cct cat gcg agg cat tca      197
45 Asp Thr Gln Thr Asn Val Leu His Asn Asp Pro His Ala Arg His Ser
46      45                  50                  55
48 gat gat aat gga cag aat cat cta gga gga caa atg aac ttc aat gca      245
49 Asp Asp Asn Gly Gln Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala
50 60                  65                  70                  75
52 gat tct agc caa cgt aaa gat gag aac aca gaa atc gct gaa aac ctc      293
53 Asp Ser Ser Gln Arg Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu
54                  80                  85                  90
```
W--> 56 tat nag caa gtt aaa att ctt tgc tgg gtt atg aca ggc tct caa aac   341
W--> 57 Tyr Xaa Gln Val Lys Ile Leu Cys Trp Val Met Thr Gly Ser Gln Asn
```
58                  95                  100                 105
60 cta cag aaa aag gcc aaa cat gtc aaa gct aca tgg gcc cag cgt tgt      389
61 Leu Gln Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys
62          110                 115                 120
```

```
 64 cta aaa gta ttt ttt atg agt tca gaa gaa aat aaa gac ttc cgt gct      437
 65 Leu Lys Val Phe Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Arg Ala
 66     125                 130             135
 68 gtg gga ttg aaa acc aaa gca ggc aga gat gag cta tac tgg aaa aca      485
 69 Val Gly Leu Lys Thr Lys Ala Gly Arg Asp Glu Leu Tyr Trp Lys Thr
 70 140             145             150             155
 72 att aac ctt ttc agtatgtt                                             505
 73 Ile Asn Leu Phe
 77 <210> SEQ ID NO: 2
 78 <211> LENGTH: 159
 79 <212> TYPE: PRT
 80 <213> ORGANISM: human
 82 <220> FEATURE:
 83 <221> NAME/KEY: misc_feature
 84 <222> LOCATION: (93)..()
 85 <223> OTHER INFORMATION: n=a, g, c or t
 87 <400> SEQUENCE: 2
 89 Met Thr Glu Asn Ser Leu Ser Glu Met Ala Ser Lys Ser Trp Leu Asn
 90 1               5               10              15
 93 Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly Phe Ile Leu Phe Ser
 94             20              25              30
 97 Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly Asp Thr Gln Thr Asn
 98         35              40              45
101 Val Leu His Asn Asp Pro His Ala Arg His Ser Asp Asp Asn Gly Gln
102     50              55              60
105 Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala Asp Ser Ser Gln Arg
106 65              70              75              80
109 Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu Tyr Xaa Gln Val Lys
110             85              90              95
113 Ile Leu Cys Trp Val Met Thr Gly Ser Gln Asn Leu Gln Lys Lys Ala
114             100             105             110
117 Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Leu Lys Val Phe Phe
118     115             120             125
121 Met Ser Ser Glu Glu Asn Lys Asp Phe Arg Ala Val Gly Leu Lys Thr
122     130             135             140
125 Lys Ala Gly Arg Asp Glu Leu Tyr Trp Lys Thr Ile Asn Leu Phe
126 145             150             155
129 <210> SEQ ID NO: 3
130 <211> LENGTH: 489
131 <212> TYPE: DNA
132 <213> ORGANISM: human
134 <220> FEATURE:
135 <221> NAME/KEY: CDS
136 <222> LOCATION: (55)..(489)
138 <400> SEQUENCE: 3
140 catctaaaaa gactgatgaa gttgattgca aatgctagtc atcataaata ccag aac      57
141                                                               Asn
142                                                               1
144 aca ggt gtc act gac aaa ctc tat caa aag atg aaa att ctt tgc tgg     105
```

W--> (at line 109)

(handwritten annotation, right of lines 83–85): → no n in sequence; must explain Xaa — see error summary sheet item 9

```
145 Thr Gly Val Thr Asp Lys Leu Tyr Gln Lys Met Lys Ile Leu Cys Trp
146              5                   10                  15
148 att atg aca gga cct caa aat cta gaa aaa aag atc aga cgc atc aga      153
149 Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile Arg
150          20                  25                  30
152 gat aca tgg gcc cag ggt tgc aat aaa gcg ttg ttt atg agc tca aaa      201
153 Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser Lys
154      35                  40                  45
156 gaa aat aaa gac ttc tct act gtg gga tta cac acc aaa gaa gac aga      249
157 Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp Arg
158 50                  55                  60                  65
160 aac caa ctg tcc tgg aaa ata gtt aaa gct ttt cta tat gct cat gac      297
161 Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His Asp
162                  70                  75                  80
164 cat tat ctg gaa tac atg gat tgg ttc atg aaa gca gat gat gat ata      345
165 His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp Ile
166              85                  90                  95
168 tgt ata tat atc aca ttg gac aac ttg aaa tgg ctt ctc aca aac tat      393
169 Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn Tyr
170          100                 105                 110
172 aac cct gat gaa tcc act tac ttt ggg aaa aga ttt aag cac tgc aga      441
173 Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys Arg
174      115                 120                 125
176 aaa cag gac tac atg act gga gga gca gga tat gta ctg agc aaa gaa      489
177 Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys Glu
178 130                 135                 140                 145
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 145
183 <212> TYPE: PRT
184 <213> ORGANISM: human
186 <400> SEQUENCE: 4
188 Asn Thr Gly Val Thr Asp Lys Leu Tyr Gln Lys Met Lys Ile Leu Cys
189 1                   5                   10                  15
192 Trp Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile
193              20                  25                  30
196 Arg Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser
197          35                  40                  45
200 Lys Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp
201      50                  55                  60
204 Arg Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His
205 65                  70                  75                  80
208 Asp His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp
209                  85                  90                  95
212 Ile Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn
213          100                 105                 110
216 Tyr Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys
217          115                 120                 125
220 Arg Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys
221          130                 135                 140
```

RAW SEQUENCE LISTING   DATE: 03/27/2002
PATENT APPLICATION: US/10/029,359A   TIME: 13:59:40

Input Set : A:\00404.sequencelist.txt
Output Set: N:\CRF3\03272002\J029359A.raw

```
224 Glu
225 145
228 <210> SEQ ID NO: 5
229 <211> LENGTH: 1560
230 <212> TYPE: DNA
231 <213> ORGANISM: human
233 <220> FEATURE:
234 <221> NAME/KEY: CDS
235 <222> LOCATION: (2)..(934)
237 <400> SEQUENCE: 5
238 a gat aat gga cag aat cat cta gaa gga caa atg aac ttc aat gca gat       49
239   Asp Asn Gly Gln Asn His Leu Glu Gly Gln Met Asn Phe Asn Ala Asp
240   1               5                   10                  15
242 tct agc caa cat aaa gat gag aac aca gac att gct gaa aac ctc tat        97
243 Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
244             20                  25                  30
246 cag aaa gtt aga att ctt tgc tgg gtt atg acc ggc cct caa aac cta       145
247 Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
248         35                  40                  45
250 gag aaa aag gcc aaa cac gtc aaa gct act tgg gcc cag cgt tgt aac       193
251 Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
252     50                  55                  60
254 aaa gtg ttg ttt atg agt tca gaa gaa aat aaa gac ttc cct gct gtg       241
255 Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
256 65                  70                  75                  80
258 gga ctg aaa acc aaa gaa ggc aga gat caa cta tac tgg aaa aca att       289
259 Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
260                 85                  90                  95
262 aaa gct ttt cag tat gtt cat gaa cat tat tta caa gat gct gat tgg       337
263 Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
264             100                 105                 110
266 ttt ttg aaa gca gat gat gac acg tat gtc ata cta gac aat ttg agg       385
267 Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
268         115                 120                 125
270 tgg ctt ctt tca aaa tac gac cct gaa gaa ccc att tac ttt ggg aga       433
271 Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg
272     130                 135                 140
274 aga ttt aag cct tat gta aag cag ggc tac atg agt gga gga gca gga       481
275 Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly
276 145                 150                 155                 160
278 tat gta cta agc aaa gaa gcc ttg aaa aga ttt gtt gat gca ttt aaa       529
279 Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys
280                 165                 170                 175
282 aca gac aag tgt aca cat agt tcc tcc att gaa gac tta gca ctg ggg       577
283 Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly
284             180                 185                 190
286 aga tgc atg gaa att atg aat gta gaa gca gga gat tcc aga gat acc       625
287 Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr
288         195                 200                 205
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RAW SEQUENCE LISTING   DATE: 03/27/2002
PATENT APPLICATION: US/10/029,359A   TIME: 13:59:40

Input Set : **A:\00404.sequencelist.txt**
Output Set: **N:\CRF3\03272002\J029359A.raw**

```
290 att gga aaa gaa act ttt cat ccc ttt gtg cca gaa cac cat tta att      673
291 Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile
292     210                 215                 220
294 aaa ggt tat cta cct aga acg ttt tgg tac tgg aat tac aac tat tat      721
295 Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr
296 225                 230                 235                 240
298 cct cct gta gag ggt cct ggt tgc tgc tct gat ctt gca gtt tct ttt      769
299 Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe
300                 245                 250                 255
302 cac tat gtt gat tct aca acc atg tat gag tta gaa tac ctc gtt tat      817
303 His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr
304                 260                 265                 270
306 cat ctt cgt cca tat ggt tat tta tac aga tat caa cct acc tta cct      865
307 His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro
308         275                 280                 285
310 gaa cgt ata cta aag gaa att agt caa gca aac aaa aat gaa gat aca      913
311 Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr
312     290                 295                 300
314 aaa gtg aag tta gga aat cct tgaaagaaaa tcatgaatga acaaaggtaa        964
315 Lys Val Lys Leu Gly Asn Pro
316 305                 310
318 tatgtctagc actgcactga aaaaggactt ctgcatttct gacatagaac actggaatcc   1024
320 cagtgaggaa ttctaagtga acattcctta tagaaacctt tcacatgaat gactataaac   1084
322 tgaagcttta aatgagctgt gaagtgtgtt aaaatgtgtt ttgatacagt aatatataaa   1144
324 tatgtctata tatatgagga acttgtgttt tttaaatggt ggccaggtag aggaactaga   1204
326 aaagagattt tgttgcctgt tttctgacca tctgtgttat tgtcactgag aaactaaaat   1264
328 agtaaattta ctaaaactac actgcaccat gttagtaata aacagatctg ccttaaagaa   1324
330 aagaaaattt tagaaagaaa tattgttgct cagtgttgtt aatatagctc aagaattgag   1384
332 tttatatttg cagtatgcta taaatgatac ccccctacca cacccacaca cacagttttt   1444
334 gtctaatgaa aatgttgctg tgattatgta taattggtag tatttcttcc agaagaagct   1504
336 aaaataagac tggcacttac cctgaagtgc attaataaaa ccacacttta aaatta        1560
339 <210> SEQ ID NO: 6
340 <211> LENGTH: 311
341 <212> TYPE: PRT
342 <213> ORGANISM: human
344 <400> SEQUENCE: 6
345 Asp Asn Gly Gln Asn His Leu Glu Gly Gln Met Asn Phe Asn Ala Asp
346 1               5                   10                  15
349 Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
350                 20                  25                  30
353 Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
354         35                  40                  45
357 Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
358     50                  55                  60
361 Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
362 65                  70                  75                  80
365 Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
366                 85                  90                  95
369 Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
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VERIFICATION SUMMARY   DATE: 03/27/2002
PATENT APPLICATION: US/10/029,359A   TIME: 13:59:41

Input Set : **A:\00404.sequencelist.txt**
Output Set: **N:\CRF3\03272002\J029359A.raw**

L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2